

FIGURE 1

CGTCCTATCTGCAGTCGGCTACTTCAGTGGCAGAAGAGGCCACATCTGCTTCCTGTAGG
CCCTCTGGCAGAACGCATGCCTGGTCTCCTCTGATCTGGGCCAGGGCTGAGGCA
GGCTCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACAAACGGGAAACATTCTGC
AGAGAAAAGTGGCTCTATCATCTTACAATGTCACCTCTCCTCCACCA CGGCACAAGTGAC
CCAGGTCAACTGGGAGCAGCAGGACAGCTCTGGCATTGTAATGCTGACTTGGGGTG
GCACATCTCCCCATCCTCAAGGATCGAGTGGCCCCAGGTCCCGCCTGGCCTCACCT
CCAGTCGCTGACCGTGAACGATAACAGGGAGTACTTCTGCATCTATCACACCTACCTGA
TGGGACGTACACTGGAGAATCTTCCTGGAGGTCTCTAGAAAGCTCAGTGGCTGAGCACGG
TGCAGGTTCCAGATTCATTGCTTGGAGCCATGGCCGCGACGCTGGTGGTATCTGCAC
AGCAGTCATCGTGGTGGTCGCGTTGACTAGAAAGAAAGCCCTCAGAATCCATTCTGT
GGAAGGTGACCTCAGGAGAAATCAGCTGGACAGGAGGAATGGAGCCAGTGCTCCCTC
ACCCCCAGGAAGCTGTGTCAGGCAGAACGCTG CACCTGCTGGCTCTGTGGAGAGCAGCG
GGGAGAGGACTGTGCCAGCTGCATGACTACTTCAATGTCCTGAGTTACAGAACGCTGGG
TAACTGCAGCTTCTTCAAGAGACTGGTTAGCAACCAGAGGCATCTTCTGG

FIGURE 2

MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE
 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTQLS LTVNDTGEYFCIYHTYPDGTYTG
 RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR
 RKSAGQE EWS PSAPS PPPGSCVQAEAAAPAGLCGEQRGEDCAELHDYFNVL SYRSLGNCSFF
 TETG

Signal sequence

1-15

Transmembrane domain

140-160

N-glycosylation site.

32-35

101-104

236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

180-183

N-myristoylation site.

21-26

25-30

31-36

90-95

116-121

144-149

Immunoglobulin domain

38-110

ITIM domain

218-228

FIGURE 3

GCCAGTTCAAGTGGAGGAGAGGCCACATCCA CTTGCTGTAGGCCTCTGGTTAGAAAGCA
TGCATGGCTGGCTGCTCTGGTCTGGGTCCAGGGCTGATA CAGGCTGCCTTCCTCGCTA
CAGGAGC CACAGCAGGCACGATAGATA CAAAGAGGAACATCTCTGCA GAGGAAGGTGGCT
CTGTCATCTTACAGTGTCACTTCTCCTCTGACACAGCTGAAGTGACC CAAGTCGACTGGA
AGCAGCA GGAC CAGCTTCTGGCCATTATAGTGTGACCTGGGTGGCATGTCGCTTCAG
TCTTCAGTGATCGGGTGGTCCCAGGCCAGCCTAGGCCTCACCTTCAGTCTCTGACAA
TGAATGA CACGGGAGAGTACTTCTGTACCTATCATACGTATCCTGGTGGGATTACAAGG
GGAGAATATTCTGAAGGTCCAAGAAAGCTCAGTGGCTCAGTTCCAGACTGCCCCGCTTG
GAGGAACCATGGCTGCTGTGCTGGGACTCATTTGCTTAATGGTCACAGGAGTGACTGTAC
TGGCTAGAAAGAGTCTATTAGAAATGCAATTCTATAGAAAGTGGCCTTGGGAGAACAGAAC
CGGAGCCACAGGAATGGAACCTGAGGAGTCCTCATCCCCCTGGAAGCCTGTCAGACAC
AAACTGCCCTGCTGGTCCCTGTGGAGAGCAGGCAGAAGATGACTATGCTGACCCACAGG
AATACTTAAATGTCCTGAGCTACAGAAGCCTAGAGAGCTTCATTGCTGTATCGAACACTG
GCTAACGACAGCTCTATCCCTCTCCCTATGTCCTCTCTCTGTCTCTCTCTCTCTCTCTCT
TCTGTCTCTGTCTCTGTCT
TGTGTGTATGTGTGTATACATCATTAAATGTTCAATTAAACTAACTGCAATGGTGGAGGA
CCAGGAAATAAAAGTTGTGTTGCTAATAAAATTAGTGCTAACTT

FIGURE 4

MHGWL₁LLVWVQGLI₂QAA₃FLATGATAGT₄IDTKRN₅ISAE₆EGGSV₇ILQCH₈FSSDTAEVTQVDW₉KQQDQLL₁₀AIYSVDLGWH₁₁VASVFSDRVVPGPSL₁₂GLTFQSLTMNDTGEY₁₃FCTYHTYPGGIYK₁₄GRIFLK₁₅VQESSV₁₆AQFQTAPL₁₇GGTMAAVLGLICL₁₈MVTGVTVL₁₉ARKKSIRMH₂₀HSIESGLGRTE₂₁AEPQEWN₂₂NLRSLS₂₃SPGSPVQTQTAPAG₂₄PCGEQA₂₅EDDYADPQ₂₆EYFN₂₇VLS₂₈YRSLES₂₉FIAV₃₀SKTG₃₁

Signal sequence

1-16

Transmembrane domain

138-158

N-glycosylation site.

33-36
102-105

Glycosaminoglycan attachment site.

174-177

cAMP- and cGMP-dependent protein kinase phosphorylation site.

163-166

N-myristoylation site.

12-17
22-27
26-31
117-122
141-146
142-147
175-180

Immunoglobulin domain

39-111

ITIM domain

221-230